18-10-680-349-42_copy_61_86.rag PW MWW W MMJ/1/06 Page 1

GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

January 24, 2006, 11:28:32; Search time 17.6732 Seconds (without alignments) 646.394 Million cell updates/sec Run on:

US-10-680-349-42_COPY_61_86

1 PINGTNSLTKKVFGLKKDGDITKKDD 26 Perfect score: Sequence:

BLOSUM62 Scoring table: 2443163 seqs, 439378781 residues Searched:

Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters:

Minimum

seq length: 0 seq length: 200000000 88

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 21:*
: geneseqp1980s:* geneseqp2000s:*geneseqp2001s:* geneseqp20028:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2005s:*

	. uo	E. canis	Ehrlichia	Ehrlichia	B. canis	Ehrlichia	 Chafee 	Ehrlichia	Ehrlichia	Bhrlichia	B. chaffe	Erlidhia	Bacterial	Protein e	Enterococ	Protein e	Bacterial	Bacterial	Cowdria r	Cowdria r	N. gonorr	z	胚	Pinus rad	Enterohae
	Description	Aay06970	Aau96116	Abg77958	Ada09781	Adw04274	Aay06944	Aau96106	Aau73413	Abg77936	Ada09737	Adw04230	Adn21449	Abu29155	Adh88024	Abu20708	Ads44601	Ad822299	Adw04295	Aau96111	Abp79144	Abp76775	Abo23592	Adw17535	Adc00818
SUMMARIES	8	AAY06970	AAU96116	ABG77958	ADA09781	ADW04274	AAY06944	4AU96106	PAU73413	ABG77936	ADA09737	ADW04230	ADN21449	ABU29155	ADH88024	ABU20708	ADS44601	ADS22299	ADW04295	4AU96111	ABP79144	ABP76775	AB023592	4DW17535	ADC00818
	<u> </u>	7	2	2	9	6	~	2	2	2	9	6	8	9	7	9	~	7 8	6	2	9	9	7	~ 6	7
	Duery Match Length DB	165	280	280	280	280	283	283	283	283	283	283	339	377	378	481	525	873	283	284	302	302	521	235	345
o#	Query Match	100.0	100.0	100.0	100.0	100.0	71.3	71.3	71.3	71.3	71.3	71.3	38.6	38.2	38.2	38.2	37.5	37.1	36.8	36.8	36.8	36.8	36.4	36.0	36.0
	Score	136	136	136	136	136	97	97	97	97	97	97	52.5	52	52	52	51	50.5	20	20	20	20	49.5	49	49
	Result No.		7	m	4	ស	9		80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Human sec	Aaw29653	AAW29653	.7	645	35.7	48.5	đ.
Human cas	Aae36781	AAE36781	9	616	35.7	48.5	44
Predicted	Abr41881	ABR41881	9	616	35.7	48.5	43
Mutant B	Adg32068	ADG32068	æ	594	35.7	48.5	42
_	Adg32050	ADG32050	Φ	585	35.7	48.5	41
Novel hum	Abg91382	ABG91382	Ŋ	557	35.7	48.5	40
_	Aau20133	AAU20133	4	557	35.7	48.5	66
Pyrococcu	Ad123827	ADL23827	œ	476	35.7	48.5	38
Pyrococcu	Abg99093	ABG99093	4	476	35.7	48.5	37
	Aaw44331	AAW44331	~	416	35.7	48.5	36
_	Aar74151	AAR74151	7	416	35.7	48.5	32
	Aab69134	AAB69134	4	2047	36.0	49	34
M. catarr	Aab69133	AAB69133	4	1992	36.0	49	33
M. catarr	Aab69137	AAB69137	4	1992	36.0	49	32
Moraxella	Aaw04505	AAW04505	~	1992	36.0	49	31
Group A 8	Adj61994	ADJ61994	œ	629	36.0	49	30
	Add68790	ADD68790	7	629	36.0	49	53
Protein e	Abu46702	ABU46702	9	577	36.0	49	28
Streptoco	Abp27646	ABP27646	ß	577	36.0	49	27
Bifidobac	Abp65734	ABP65734	Ŋ	511	36.0	49	56
-	Adn46936	ADN46936	100	4/2	36.0	49	7

ALIGNMENTS

AAY06970 standard; protein; 165 AA

AAY06970;

(first entry) 05-JUL-1999

S. canis P30-10protein.

Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog

Shrlichia canis.

25-MAR-1999.

WO9913720-A1.

*

98WO-US019600. 18-SEP-1998; 97US-0059353P. 19-SEP-1997;

OHIS) UNIV OHIO STATE

Rikihisa Y, Ohashi N;

WPI; 1999-254290/21.

N-PSDB; AAX34770

Novel outer membrane proteins from Bhrlichia chaffeensis and Bhrlichia canis.

Disclosure, Fig 30B; 55pp; English.

The invention provides isolated outer membrane proteins (OMP) from Bhrlichia chafeensis and B. canis. The B. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAX06943-958. The B. canis proteins form part of the P30 family and consist of proteins shown in AAX06959-970. The proteins and genes are used to detect B. chaffeensis in patients and B. canis in dogs AAYO6970

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Sequence 165 AA;

0; Gaps Query Match

100.0%; Score 136; DB 2; Length 165;

Best Local Similarity 100.0%; Pred. No. 2.5e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0;

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Bhrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.
PINGTNSLTKKVPGLKKDGDITKKDD
        61 PINGTNSLTKKVPGLKADGDITKADD
                                         AAU96116 standard; protein; 280 AA.
                                                                                                                                                                                    Yu X, Mcbride JW,
                                                                                                                                              12-SEP-2001; 2001WO-US028759
                                                                                                                                                          12-SEP-2000; 2000US-00660587
                                                                    (first entry)
                                                                               Bhrlichia canis p28-2.
                                                                                                                                                                       (RERE-) RES DEV FOUND
                                                                                                                                                                                              WPI; 2002-351882/38.
N-PSDB; ABK68876.
                                                                                                        Ehrlichia canis.
                                                                                                                     WO200222782-A2
                                                                  02-JUL-2002
                                                                                                                                  21-MAR-2002.
                                                                                                                                                                                  Walker DH,
                                                      AAU96116;
                                    AAU961.
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          a
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The invention relates to a recombinant homologous 28 kDa immunodominant protein, P28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting B. canis infection in a subject. (I) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. AAUSGIO0-AAUSGII8 represent the 28-kDa antigen amino acid sequences of the invention New recombinant homologous 28 kilodalton immunodominant protein from Ehrlichia canis, useful for treating Ehrlichia canis infections. Claim 16; Fig 14; 106pp; English

Sequence 280 AA;

Length 280; Indels , DB 5; 4.8e-12; 100.0%; Score 136; I 100.0%; Pred. No. 4.8 ive 0; Mismatches Query Match Best Local Similarity 100. Matches 26; Conservative ઠ

Gaps

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1 PINGTNSLTKKVFGLKKDGDITKKDD 26 PINGINSLIKKVPGLKKDGDIIKKDD 86

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ABG77958 standard; protein; 280 RESULT 3

ABG77958

15-NOV-2002 (first entry)

Ehrlichia canis outer membrane protein (P30F) #9

Outer membrane protein; OMP; P30F; ehrlichiosis; infection.

Ehrlichia canis.

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US2002120115-A1
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56

29-AUG-2002

28-JAN-2002; 2002US-00059964.

99US-00314701. (RIKI/) RIKIHISA Y. 19-MAY-1999;

(OHAS/) OHASHI N

Rikihisa Y, Ohashi N;

WPI; 2002-618954/66 N-PSDB; ABS63299 Isolated polynucleotide encoding an outer membrane protein of E.canis or E.chaffeensis used in the diagnosis of infection.

Claim 10; Fig 30B; 49pp; English.

The invention relates to an isolated polynuclectide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used in the diagnosis of infection. An infection such as human ehrlichiosis or canine ehrlichiosis can be diagnosed by providing a serum sample from the patient, providing a polypeptide or mixture of polypeptides, contacting the sample with the polypeptide and assaying for the formation of a complex between antibodies in the serum sample and the polypeptide, where formation of a complex is indicative of infection with E. chaffeensis. This sequence represents an Ehrlichia outer membrane protein of the

Sequence 280 AA;

; 0 Length 280; Indels Score 136; DB 5; Pred. No. 4.8e-12; Mismatches . 100.0%; 100.0%; 26; Conservative Similarity Query Match Local Matches

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Gaps

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ADA09781 standard; protein; 280 AA.

ADA09781;

(first entry) 06-NOV-2003

monocytic ehrlichiosis; membrane protein; circulating leukocyte; monocytic el Mountian spotted fever; canine ehrlichiosis; antigen B. canis outer membrane protein P30-10. Outer

Shrlichia canis.

US6544517-B1,

08-APR-2003,

99US-00314701 19-MAY-1999;

98US-0100843P. 8-SEP-1998;

(OHIS) UNIV OHIO STATE RES. FOUND.

Rikihisa Y, Ohashi N;

WPI; 2003-553952/52. N-PSDB; ADA09780.

Sequence 283 AA

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177
                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                         9
                                                                           1 MNYKKIFVSSALISLMSILPYQSFADPVTSNDTGINDSREGFYISVKYNPSISHFRKFSA
                                                                                                                                   1 MNYKKILVRSALISLMSILPYQSFADPVGSR----TNDNKEGFYISAKYNPSISHFRKFSA
                                                                                                                   58 RETPINGTNSLTKKVFGLKKOGDITKKODPTRVAPGIDFONNLISGFSGSIGYSMDGPRI
                                                                                                                                                                             118 ELEAAYQQFNPKNTDNNDTDNGEYYKHFALSRKDAMEDQQYVVLKNDGITFMSLAVNTCY
                                                                                                                                                                                                                                         DITARGVSPVPYACAGIGADLITIFKDLNLKPAYQGKIGISYPITPEVSAFIGGYYHGVI
                               Gapa
                             .
.
 DB 6; Length 283;
82.3%; Score 1202.5; DB 6; Length
79.5%; Pred. No. 3e-112;
ive 26; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                    GNNFNKIPVIIPVVLEGAPQTTSALVTIDTGYFGGEVGVRFTF 283
                                                                                                                                                                                                                                                                                                 GNKPEKIPVITPVVLMDADQTTSASVTLDVGYPGGEIGÜRFTF
 Query Match 82.3
Best Local Similarity 79.5
Matches 225; Conservative
                                                                                                                                                   19
                                                                                                                                                                                                                                         178
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ADW04230 standard; protein; 283 AA 24-MAR-2005 (first entry) Brlichia chaffeensis outer membrane protein (OMP), OMP-1B.

DNA purification; diagnosis; outer membrane protein; OMP; P30F protein; infection; vaccine.

Shrlichia chaffeensis.

/note= "Erlichia chaffeensis mature OMP protein" 82. .94 /note= "Hypervariable region (HV1)" 'note= "Hypervariable region (HV3)" 145. .163 /note= "Hypervariable region 248. .272 26. .41 /note= "Semivariable region 82. .94 .25
 /label= Signal_peptide Location/Qualifiers . 283 Key Peptide Protein Region Region Region Region

US2004265334-A1

29-JUL-2004; 2004US-00901774 30-DEC-2004

18-SEP-1998; 98US-0100843P. 19-MAY-1999; 99US-00314701. 28-JAN-2002; 2002US-00059964.

(RIKI/) RIKIHISA Y. (OHAS/) OHASHI N.

Rikihisa Y, Ohashi N;

WPI; 2005-064871/07. N-PSDB; ADW04229.

9 New polynucleotide encoding an outer membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis, useful in preparing a composition for diagnosing or preventing E. canis or E. chaffeensis infection. The invention relates to nucleic acid sequences encoding outer membrane proteins (OMP) of Erlichia chaffeensis (designated as OMP proteins) and Ehrlichia canis (designated as P30F proteins). The OMP polymocleotide is useful in preparing a composition for diagnosing, treating or preventing an infection with Ehrlichia canis or Ehrlichia chaffeensis. The present sequence is the Erlichia chaffeensis OMP protein. 1 MNYKKILVRSALISLMSILPYQSPADPVGSR---TNDNKEGFYISAKYNPSISHFRKFSA 1 MNYKKIFVSSALISIASILPYQSPADPVTSNDTGINDSREGFYISVKYNPSISHFRKFSA 58 BETPINGTNSLTKKVPGLKKDGDITKKDDPTRVAPGIDPQNNLISGFSGSIGYSMDGPRI 118 ELEAAYQQFNPKNTDNNDTDNGEYYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTCY DITARGUSFVPYACAGIGADLITIFKOLNLKFAYQGKIGISYPITPEVSAFIGGYYHGVI Gaps DB 9; Length 283; Query Match 82.3%; Score 1202.5; DB 9; Length Best Local Similarity 79.5%; Pred. No. 3e-112; Matches 225; Conservative 26; Mismatches 29; Indels GNKFEKIPVITPVVLNDAPQTTSASVTLDVGYFGGBIGMRFTF 280 GNNFNKIPVITPVVLEGAPQTTSALVTIDTGYFGGEVGVRFTF 283 Disclosure, SRQ ID NO 4; 122pp; English Sequence 283 AA; 238 178 241 셤 셤 셤 ò 셤 ò 8 ઠે 8

05-JUL-1999 (first entry) E. canis P30-10protein AAY06970;

AAY06970 standard; protein; 165 AA.

AAY06970

membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; 97US-0059353P Shrlichia canis. detection; dog WO9913720-A1 18-SEP-1998; 19-SEP-1997;

(OHIS) UNIV OHIO STATE

Ohashi N;

Rikihisa Y,

Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia WPI; 1999-254290/21 N-PSDB; AAX34770. canis. 7

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and B. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAX06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAX06959-970. The proteins and genes are used to detect E. chaffeensis in patients and B. canis in dogs Disclosure; Fig 30B; 55pp; English.

Sequence 165 AA;

12; Gaps 48.9%; Score 715; DB 2; Length 165; ilarity 81.9%; Pred. No. 1.8e-63; Conservative 4; Mismatches 16; Indels 1 Local Similarity Best Local Sim Matches 145; Query Match

9 MNYKKILVRSALISLMSILPYQSFADPVGSRTNDNKBGFYISAKYNPSISHFRKFSARET MNYKKILVRSALISLMSILPYQSFADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAEET Н

PINGTNSLTKKVPGLKKDGDITKKDDFTRVAPGIDPQNNLISGFSGSIGYSMDGPRIBLE 120 PINGTNSLTKKVFGLKKDGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMDGPRIELE 120 61

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121 AAYQQFNPKNTDNNDTDNGEYYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTCY 177

RESULT 12

AAY06943 standard; protein; 281 AA

AAY06943;

(revised)
(first entry) 27-AUG-2003 05-JUL-1999

B. chafeensis OMP-1 protein

Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog

Rhrlichia chaffeensis.

WO9913720-A1

25-MAR-1999

98WO-US019600 18-SEP-1998;

97US-0059353P 19-SEP-1997;

(OHIS) UNIV OHIO STATE

Rikihisa Y, Ohashi N;

WPI; 1999-254290/21. N-PSDB; AAX34743.

Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia Disclosure; Fig 3B; 55pp; English. canis.

The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs. (Updated on 27-AUG-2003 to correct OS field.) AAY06943

XX AAX0

XX Bhrl

XX AAX0

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PRIELEAAYQQFNPKWTDNNDTDNGEYYKHFALSRKDAME----DQQYVVLKNDGITFMS 170
                                                                                                                                                                                                         LAVNICYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPITPEVSAFIG 230
                                                                                                                                                                                                                                                              61 PINGTNSLTXKVPGLKKODGD-----ITKKDDFTRVAPGIDPONNLISGFSGSIGYSMDG 114
                                                                                              1 MNYKKVFITSALISLISSLPGVSFSDPAGSGINGN---FYISGKYMPSASHFGVFSAKB-
                                                                                1 MNYKKILVRSALISLMSILPYQSPADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAERT
                                                       Gaps
                                                      21;
                           Length 281;
                                                                                                                                                                                                                                                                                                                   GYYHGVIGNKFEKIPVITPVVLNDAPQ-TTSASVTLDVGYFGGEIGMRFTF
              44.1%; Score 644.5; DB 2; Lenyum -48.1%; Pred. No. 5e-56;
                                                   Matches 140; Conservative
                      Query Match
Best Local Similarity
Sequence 281 AA;
                                                                                                                                                             57
                                                                                                                                                                                                                    113
                                                                                                                                                                                                                                                                                                    231
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AAU96105

AAU96105 standard; protein; 281 AA

AAU96105;

(revised)
(first entry) 07-AUG-2003 02-JUL-2002

Shrlichia chafeensis P28

Shrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial

Shrlichia chaffeensis

WO200222782-A2

21-MAR-2002.

12-SEP-2001; 2001WO-US028759

.2-SEP-2000; 2000US-00660587

(RERE-) RES DEV FOUND

Mcbride JW Yu X, Walker DH,

WPI; 2002-351882/38.

New recombinant homologous 28 kilodalton immunodominant protein from Ehrlichia canis, useful for treating Ehrlichia canis infections.

Example 3; Fig 3; 106pp; English

The invention relates to a recombinant homologous 28 kDa immunodominant protein, P28, (I), of Shrlichha canis. (I), a 28-kDa antigen preferably dispersed in a pharmaceutically acceptable carrier, is useful for inhibiting B. canis infection in a subject. (I) is useful in the development of vaccines and serodiagnostics that are particularly effective for disease prevention and serodiagnosis. AAU96100-AAU96118 represent the 28-kDa antigen amino acid sequences of the invention. (Updated on 07-AUG-2003 to correct OS field.)

Sequence 281

Query Match

DB 5; Length 281 44.1%; Score 644.5;